AMENDMENTS TO THE CLAIMS:

This listing of the claims will replace all prior listings and versions of claims in the application:

1-2 (cancelled)

3. (currently amended) A system for predicting nucleic acid three-dimensional structure, comprising a processor configured to:

a) compute a plurality of secondary structures of a test nucleic acid;

b) decompose said secondary structures into nucleic acid structure motifs;

c) rank said structure motifs in a hierarchal tree;

d) identify candidate three-dimensional motif structures for said motifs from a database of known three-dimensional structure motifs;

e) link said candidate three-dimensional motif structures in an order specified by said hierarchal tree to generate a candidate three-dimensional composite structure;

f) submit said candidate three-dimensional composite structure to an energy minimization algorithm to generate one or more refined candidate three-dimensional structure;

g[[.]]) rank said one or more refined candidate three-dimensional structures based on the calculated total energy and optionally one or more scoring parameters comprising: solvent accessible surface area, molecular density, non-bonded energy; and

h) select a refined candidate three-dimensional structure based on best calculated energy to predict a three-dimensional structure of said test nucleic acid.

4. (original) A method for generating a three-dimensional structure of a test nucleic acids, comprising the step of submitting a test sequence to the system of claim 3 under conditions such that a three-dimensional structure of said test sequence is generated.

5.   (original) A system for generating a nucleic acid structure motif database, comprising a processor configured to:

    a)   receive nucleic acid physical structure information;

    b)   decompose said physical structure information into nucleic acid structure motifs;

    c)   associate data with said structure motifs, said data comprising: type of motif, size of motif, coordinates of backbone, and dihedral angles for bases;

    d)   compare said nucleic acid structure motifs to existing motifs in said database; and

    e)   add said structure motif and associate data to said database.

6.   (original) A method for generating a nucleic acid structure motif database, comprising the step of submitting nucleic acid physical structure information to the system of claim 5.

7-10 (cancelled)